

STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 128112

TO: Karen A Lacourciere

Location:

Art Unit: 1635

July 26, 2004

Case Serial Number: 09/301380

From: P. Sheppard

Location: Remsen Building

Phone: (571) 272-2529

sheppard@uspto.gov

Search Notes

Sheppard, Paula

18 2/12

From: Lacourciere, Karen
Sent: Wednesday, July 21, 2004 3:48 PM
To: Sheppard, Paula
Subject: RE: Sequence search

Hi Paula-
The numbers are
ABA70229
AAI50358
AAK44359
AAK18454
ABS44016
ABS18595
ABA71469
AAI51738
AAK45811

The serial number is 09/301,380 and the sequence these oligos bind to is SEQ ID NO:1
I can bring the original search down to you if it helps. Let me know what you need! Thanks so much, I really appreciate your help.
Karen

-----Original Message-----

From: Sheppard, Paula
Sent: Tuesday, July 20, 2004 5:28 PM
To: Lacourciere, Karen
Subject: RE: Sequence search

Yes. If you can provide the accession numbers of interest and the seq ID used to search it, then I can provide you with alignments and references.

Paula
(571) 272-2529

-----Original Message-----

From: Lacourciere, Karen
Sent: Tuesday, July 20, 2004 2:53 PM
To: Sheppard, Paula
Subject: Sequence search

Hi Paula-
You did a sequence search for me back in May on SN 301,380. Some of the hits which appear in the summary now appear to be potentially useful references, but they are too far down on the list and the detailed summaries were not provided. Is it possible to get more information on these sequences based on the accession numbers?
Thanks-
Karen

Karen A. Lacourciere Ph.D.

Remsen 2D15 GAU 1635
(571) 272-0759

> O <
O| | O IntelliGenetics
> O <

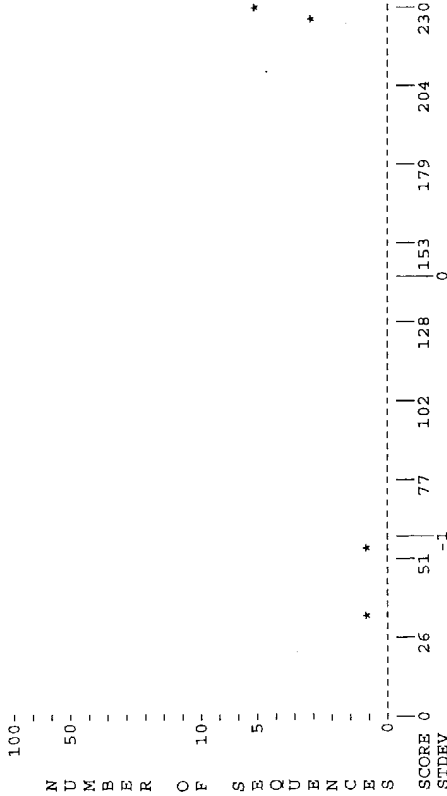
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file 1_x_listing_inv.res made by spaula on Mon 26 Jul 104 14:24:17-PDT.

Query sequence being compared:US-09-301-380-1' (1-4134)
Number of sequences searched: 8
Number of scores above cutoff: 8

Results of the initial comparison of US-09-301-380-1' (1-4134) with:

File : aal50358.seq
File : aal51738.seq
File : aak18454.seq
File : aak44359.seq
File : aak45811.seq
File : aak45911.seq
File : abs44016.seq
File : abs18595.seq



PARAMETERS

Similarity matrix Unitary K-tuple
Mismatch penalty 1.00 Joining penalty 4
Gap penalty 0.33 Window size 30
Gap size penalty 0.33
Cutoff score 0
Randomization group 0

SEARCH STATISTICS

Scores: Mean 182 Median 225 Standard Deviation 84.92
Times: CPU 00:00:00.90 Total Elapsed 00:00:00.00
Number of residues: 2676
Number of sequences searched: 8
Number of scores above cutoff: 8

The scores below are sorted by initial score.

Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Init. Opt.	Sig. Frame
1. aak18454	Human brain expressed single	230	230	230	0.57
2. aak44359	Human bone marrow expressed s	230	230	230	0.57
3. abs18595	Human genome-derived single e	230	230	230	0.57
4. abs44016	Human liver single exon probe	230	230	230	0.57
5. aak45811	Human bone marrow expressed s	224	224	224	0.49
6. abs471469	Human foetal liver single exo	224	224	224	0.49
7. aal50358	TOIG of: aal50358 check: 446	611	55	289	-1.50
8. aal51738	TOIG of: aal51738 check: 878	697	35	287	-1.73

1. US-09-301-380-1' (1-4134)
aak18454 Human brain expressed single exon probe SEQ ID NO:

TOIG of: aak18454 check: 7397 from: 1 to: 230

ID AAK18454 standard; DNA; 230 BP.
XX AC AAK18454;
XX DT 05-NOV-2001 (first entry)
XX DE Human brain expressed single exon probe SEQ ID NO: 18445.
XX KW Human; brain expressed exon; gene expression analysis; probe; microarray;
XX KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
XX OS Homo sapiens.
XX PN WO200157275-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000667.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX PA Penn SG, Hanzel DK, Chen W, Rank DR;
XX PI MPI; 2001-483446/52.
XX DR
XX PT Single exon nucleic acid probes for analyzing gene expression in human
XX PT brains.
XX PS Example 4; SEQ ID NO 18445; 650pp + Sequence Listing; English.
XX CC The present invention provides a number of single exon nucleic acid
XX CC probes which are derived from genomic sequences expressed in the human
XX CC brain. They can be used to measure gene expression in brain cell samples,
XX CC which may enable the diagnosis and improved treatment of nervous system
XX CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX CC epilepsy and cancers. The present sequence is one of the probes of the
XX CC invention

XX PN W0200186003-A2.
XX PD 15-NOV-2001.
XX PF 30-JAN-2001; 2001WO-US000665.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX DR WPI; 2002-114183/15.
XX PT Spatially-addressable set of single exon nucleic acid probes, used to
XX PT measure gene expression in human lung samples.
XX PS Claim 4; SEQ ID NO 18586; 63app; English.
XX CC The invention relates to a spatially-addressable set of single exon
XX CC nucleic acid probes for measuring gene expression in a sample derived
XX CC from human lung comprising single exon nucleic acid probes having one of
XX CC 12614 nucleic acid sequences mentioned in the specification, or their
XX CC complements or the 12387 open reading frames derived from the 12614
XX CC probes. Also included are a microarray comprising the novel set of probes
XX CC; the novel set of probes which hybridise at high stringency to a nucleic
XX CC acid expressed in the human lung; measuring gene expression in a sample
XX CC derived from human lung, comprising (a) contacting the array with a
XX CC collection of detectably labeled nucleic acids derived from human lung
XX CC mRNA, and (b) measuring the label detectably bound to each probe of the
XX CC array; identifying exons in a eukaryotic genome, comprising (a)
XX CC algorithmically predicting at least one exon from genomic sequences of
XX CC the eukaryote; and (b) detecting specific hybridisation of detectably
XX CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
XX CC having a fragment identical to the predicted exon, the probe is included
XX CC in the above mentioned microarray; assigning exons to a single gene,
XX CC comprising (a) identifying exons from genomic sequence by the method
XX CC above and (b) measuring the expression of each of the exons in several
XX CC tissues and/or cell types using hybridisation to a single exon
XX CC microarrays having a probe with the exon, where a common pattern of
XX CC expression of the exons in the tissues and/or cell types indicates that
XX CC the exons should be assigned to a single gene; a peptide comprising one
XX CC of 12011 sequences, mentioned in the specification, or encoded by the
XX CC probes/open reading frames (ORF). The probes are used for gene expression
XX CC analysis, and for identifying exons in a gene, particularly using human
XX CC lung derived mRNA and for the study of lung diseases such as asthma, lung
XX CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
XX CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
XX CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
XX CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
XX CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
XX CC Karagenen syndrome, fibrocystic pulmonary dysplasia, primary ciliary
XX CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
XX CC present sequence is a single exon probe open reading frame of the
XX CC invention. Note: The sequence data for this patent did not form part of
XX CC the printed specification, but was obtained in electronic format directly
XX CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 230 BP; 45 A; 61 C; 44 G; 80 T; 0 U; 0 Other;
ABS18595 Length: 230 July 26, 2004 14:11 Type: N Check: 7397 ..
Initial Score = 230 Optimized Score = 230 Significance = 0.57
Residue Identity = 100% Matches = 230 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

70 80 90 100 110 120 130
AAACATTCAGAGAAATGGAATATTGGCTTTGAGCTTAAATAATTAACAAGGAATTCATGGCGTTGACAGG
|||||
AGGAATTCATGGCGTTGACAGG
X 10 20
140 150 160 170 180 190 200
AGAGGTGCTCTGAGCTTTTCCTTTCAGCCGGCTCTTTCTCTTTTACCACTGATTGTCCAATAAA
|||||
AGAGGTGCTCTGAGCTTTTCCTTTCAGCCGGCTCTTTCTCTTTTACCACTGATTGTCCAATAAA
30 40 50 60 70 80 90
210 220 230 240 250 260 270
GGAGCCATCCTCATTTGAACCTGGCCATTAAACCCCTTCTCATAGTCAACTAGGCTGTCGTCACATCTTT
GGAGCCATCCTCATTTGAACCTGGCCATTAAACCCCTTCTCATAGTCAACTAGGCTGTCGTCACATCTTT
100 110 120 130 140 150 160
280 290 300 310 320 330 340 X 350
TTTTCAGTCCCTGCTGAAGGAGTTGAGCTTCTTTTTCAAAGGCTTGTGCTTCTGTCACATCTTT
TTTTCAGTCCCTGCTGAAGGAGTTGAGCTTCTTTTTCAAAGGCTTGTGCTTCTGTCACATCTTT
170 180 190 200 210 220 230
TCCAAATGCCCATCATCTTCTTCATAGGCTGGATTTCAGG
360 370 380 390

4. US-09-301-380-1' (1-4134)
abs44016 Human liver single exon probe, SEQ ID NO 19006.

TOIG of: abs44016 check: 7397 from: 1 to: 230

ID ABS44016 standard; DNA; 230 BP.
XX AC ABS44016;
XX AC
XX DT 25-FEB-2003 (first entry)
XX DE Human liver single exon probe, SEQ ID NO 19006.
XX KW Human; single exon nucleic acid probe; liver; cirrhosis;
XX KW hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
XX KW coronary heart disease; ss.
XX OS Homo sapiens.
XX PN W0200157273-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000664.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX FA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX DR WPI; 2001-488898/53.
XX PT Human genome-derived single exon nucleic acid probes useful for analyzing
XX PT gene expression in human adult liver.
XX PS Claim 4; SEQ ID NO 19006; 658pp; English.
XX CC The invention relates to a single exon nucleic acid probe (SENp) (I) for

CC measuring human gene expression in a sample derived from human adult
CC liver, comprising one of 13109 defined nucleotide sequences given in the
CC specification (or complements/ fragments). The probe hybridises at high
CC stringency to a nucleic acid molecule expressed in the human adult liver.
CC (1) may be used for predicting, measuring and displaying gene expression
CC in samples derived from human adult liver. The genes identified may be
CC involved in genetic liver diseases such as cirrhosis,
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
CC associated with coronary heart disease. ABS25011-ABS51005 represent human
CC liver single exon nucleic acid probes of the invention. Note: The
CC sequence information for this patent does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 230 BP; 45 A; 61 C; 44 G; 80 T; 0 U; 0 Other;

ABS44016 Length: 230 July 26, 2004 14:11 Type: N Check: 7397 ..

Initial Score = 230 Optimized Score = 230 Significance = 0.57
Residue Identity = 100% Matches = 230 Mismatches = 0
Gaps = 0 Conservative Substitutions

70 80 90 100 110 120 130
AAACATCTAGAGAAATGGATATGGCTTTGAGCTTAAATAATTAACAAGGAATTCATGGCTTGACAGG
|||||
AGGAATTCATGGCGTTGACAGG
X 10 20

140 150 160 170 180 190 200
AGAGGTGCTCTGAGCTTTCCTTCCTGACCGGCTCTTCTTCTTACACATGATTTGCCAATAAA
|||||
AGAAAGTGGCTCTGAGCTTTCCTTCCTGACCGGCTCTTCTTCTTACCACTGATTTGCCAATAAA
30 40 50 60 70 80 90

210 220 230 240 250 260 270
GGAGCCATCTCATGTAAGTGGCAATTAACCCCTTCCATAGCACTAGGCTGTGCTACTATCTCTTT
GGAGCCATCTCATGTAAGTGGCAATTAACCCCTTCCATAGCACTAGGCTGTGCTACTATCTCTTT
100 110 120 130 140 150 160

280 290 300 310 320 330 340 X 350
TTTCACAGTCTGCTCAGAGAGTTCGACTTCCTTTTCAAGGCTTGCTGCTCTGCTACTGTATTC
|||||
TTTCACAGTCTGCTCAGAGAGTTCGACTTCCTTTTCAAGGCTTGCTGCTCTGCTACTGTATTC
170 180 190 200 210 220 230

TCCAAATGTCCTCATCTCTTCCATAGGCTGGATTCAGG

5. US-09-301-380-1' (1-4134)

aak45811 Human bone marrow expressed single exon probe SEQ

TOIG of: aak45811 check: 7602 from: 1 to: 224

ID AAK45811 standard; DNA; 224 BP.

XX AAK45811;

XX 06-NOV-2001 (first entry)

XX Human bone marrow expressed single exon probe SEQ ID NO: 20368.

XX Human; bone marrow expressed exon; gene expression analysis; probe;
XX microarray; cancer; leukaemia; lymphoma; myeloma; ss.

XX Homo sapiens.

XX WO200157276-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000668.

XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488900/53.
DR Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human bone marrow.

XX Example 4; SEQ ID NO 20368; 658pp + Sequence Listing; English.

XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX bone marrow. They can be used to measure gene expression in bone marrow
XX samples, which may enable the improved diagnosis and treatment of cancers
XX such as lymphoma, leukaemia and myeloma. The present sequence is one of
XX the probes of the invention

XX SQ Sequence 224 BP; 58 A; 59 C; 49 G; 58 T; 0 U; 0 Other;

AAK45811 Length: 224 July 26, 2004 14:11 Type: N Check: 7602 ..

Initial Score = 224 Optimized Score = 224 Significance = 0.49
Residue Identity = 100% Matches = 224 Mismatches = 0
Gaps = 0 Conservative Substitutions

1450 1460 1470 1480 1490 X 1500 1510
TACTGTTCACCAATTCACAGCAGTTCACGAGGCCACCATTTGGAGGCTCTTCTCAGAAATGCCCATGA
|||||
TCTTCTCCAGAAATGCCCATGA
X 10 20

1520 1530 1540 1550 1560 1570 1580
CTACAGCTGGCTCGGGGGCAAAACCCCATGTCATTCAGGGCTGAACCTTGTATGATGATGATGAACAAAGGTTG
|||||
CTACAGCTGGCTCGGGGGCAAAACCCCATGTCATTCAGGGCTGAACCTTGTATGATGATGATGAACAAAGGTTG
30 40 50 60 70 80 90

1590 1600 1610 1620 1630 1640 1650
GCGTGCTGTAGACAAATATTTGGATACATTTGCCAACACACAGATGTCATTCATCATCACCATCTTTCT
|||||
GCGTGCTGTAGACAAATATTTGGATACATTTGCCAACACACAGATGTCATTCATCATCACCATCTTTCT
100 110 120 130 140 150 160

1660 1670 1680 1690 1700 1710 1720 1730
GGGCCAGCTAACTTTGTACTGAGAGGCTGCCCCATTAAGATTCGAAACCATTCAGGCTTCCACGTAATCT
|||||
GGGCCAGCTAACTTTGTACTGAGAGGCTGCCCCATTAAGATTCGAAACCATTCAGGCTTCCACGTAATCT
170 180 190 200 210 220 X

CCAAATATCAGGCTCTGATCCCGAGTCTTCCACAG

6. US-09-301-380-1' (1-4134)

aba71469 Human foetal liver single exon nucleic acid probe

TOIG of: aba71469 check: 7602 from: 1 to: 224

ID ABA71469 standard; DNA; 224 BP.

XX ABA71469;

XX 01-FEB-2002 (first entry)

XX DE Human foetal liver single exon nucleic acid probe #19774.
XX KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX OS Homo sapiens.
XX FN WO200157277-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000669.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483447/52.
XX DR Human genome-derived single exon nucleic acid probes useful for analyzing
XX PT gene expression in human fetal liver.
XX PS Claim 4; SEQ ID NO 19774; 639pp + Sequence Listing; English.
XX CC The invention relates to a single exon nucleic acid probe for measuring
XX CC human gene expression in a sample derived from human foetal liver. The
XX CC single exon nucleic acid probes may be used for predicting, measuring and
XX CC displaying gene expression in samples derived from human fetal liver. The
XX CC present sequence is a single exon nucleic acid probe of the invention.
XX CC Note: The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 224 BP; 58 A; 59 C; 49 G; 58 T; 0 U; 0 Other;

ABA71469 Length: 224 July 26, 2004 14:11 Type: N Check: 7602 ..
Initial Score = 224 Optimized Score = 224 Significance = 0.49
Residue Identity = 100% Matches = 224 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0
1450 1460 1470 1480 1490 X 1500 1510
TACTGTTCACCAATTCACAGCAGCTGCCAGGACCACCATGGAGGTCTTCCAGAAATGCCCATGA
|||||
X 10 20
1520 1530 1540 1550 1560 1570 1580
CTACAGCTGGCTCGGGGMAACCCCATGTCAATCAGGCGCTGAATTTGATCAGGTATGGAACAAGTTG
|||||
CTACAGCTGGCTCGGGGMAACCCCATGTCAATCAGGCGCTGAATTTGATCAGGTATGGAACAAGTTG
30 40 50 60 70 80 90
1590 1600 1610 1620 1630 1640 1650
GGGTGCTGAGCAATATATTGGATACATTTGCCCAACACACAGATGTCCATTCATCATCACCATTCTCT
|||||
GGGTGCTGAGCAATATATTGGATACATTTGCCCAACACACAGATGTCCATTCATCATCACCATTCTCT
100 110 120 130 140 150 160
1660 1670 1680 1690 1700 1710 1720 1730
GGGCGAGCTAACTTTGTAAGGCTGGCCCATAGATTCGAACCAATTCGAAGGCTTCCACGTAATCT
|||||
GGGCGAGCTAACTTTGTAAGGCTGGCCCATAGATTCGAACCAATTCGAAGGCTTCCACGTAATCT
170 180 190 200 210 220 X

1740 1750 1760
CCAAATTATCAGGCTCTGATCCCGAGTCTTCACAG
7. US-09-301-380-1' (1-4134)
aai50358 TOIG of: aai50358 check: 4462 from: 1 to: 611
TOIG of: aai50358 check: 4462 from: 1 to: 611
LOCUS AAI50358 611 bp mRNA linear EST 14-MAY-1997
DEFINITION z107a03.r1 Soares pregnant uterus_NbHPU Homo sapiens cDNA clone
IMAGE:491596 5', mRNA sequence.
ACCESSION AAI50358
VERSION AAI50358.1 GI:1721870
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 611)
AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,N.,
Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J.,
Trevaskis,E., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R.
and Maria,M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
889549
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 1102 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 328.

FEATURES
Location/Qualifiers
1..611
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3806183"
/db_xref="taxon:9606"
/clone="IMAGE:491596"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="Soares_pregnant_uterus_NbHPU"
/note="Organ: uterus; Vector: pT7T3-Pac; Site 1: Not I;
Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer [5',
AACTGGAGAAATTCGCGCGCGCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization. Library
constructed by M. Fatima Bonaldo."

ORIGIN
AAI50358 Length: 611 July 26, 2004 14:10 Type: N Check: 4462 ..
Initial Score = 55 Optimized Score = 289 Significance = -1.50
Residue Identity = 50% Matches = 391 Mismatches = 212
Gaps = 175 Conservative Substitutions
2860 2870 2880 2890 2900 X 2910 2920
TTTGGGTTGCCATTAGCTCTGCAGATCAAGGTCCCATCTCTCTGGGACAGACACAGATTGTAGGGGC
|||||

```
8. US-09-301-380-1' (1-4134)
aai51738 TOIG of: aai51738 check: 8787 from: 1 to: 697

TOIG of: aai51738 check: 8787 from: 1 to: 697

LOCUS      AAI51738          697 bp      mRNA      linear      EST 14-MAY-1997
DEFINITION z128h03.r1 Soares pregnant_uterus_NbHPU Homo sapiens cDNA clone
IMAGE:503285 5' similar to contains element MER22 repetitive
element ;, mRNA sequence.
ACCESSION  AAI51738
VERSION     AAI51738.1  GI:1720293
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 697)
AUTHORS     Hillier, L., Lennon, G., Becker, M., Bonaldo, M.P., Chiapelli, B.,
Chissoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W.,
Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, N.,
Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,
Trevasakis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R.
and Marra, M.
TITLE       Generation and analysis of 280,000 human expressed sequence tags
JOURNAL     Genome Res. 6 (9), 807-828 (1996)
MEDLINE     97044478
PUBMED      8889549
COMMENT     Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LBNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 813 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 513.
Location/Qualifiers
1..697
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3808273"
/db_xref="taxon:9606"
/clone="IMAGE:503285"
/sex="female"
/lab_host="DH10B"
/clone_lib="Soares_pregnant_uterus_NbHPU"
/note="Organ: uterus; Vector: pT7T3-Pac; Site 1: Not I;
Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer [5',
AACTGGGAAGAATTCGGCGCGCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization. Library
constructed by M. Fatima Bonaldo."

FEATURES             source
source
1..697
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3808273"
/db_xref="taxon:9606"
/clone="IMAGE:503285"
/sex="female"
/lab_host="DH10B"
/clone_lib="Soares_pregnant_uterus_NbHPU"
/note="Organ: uterus; Vector: pT7T3-Pac; Site 1: Not I;
Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer [5',
AACTGGGAAGAATTCGGCGCGCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization. Library
constructed by M. Fatima Bonaldo."

ORIGIN
AAI51738 Length: 697 July 26, 2004 14:11 Type: N Check: 8787 ..
Initial Score = 35 Optimized Score = 287 Significance = -1.73
Residue Identity = 45% Matches = 376 Mismatches = 305
Gaps = 148 Conservative Substitutions = 0
1470 1480 1490 1500 1510 1520 1530
CAGGTCCAGAGCACCACCATTTGGGAGGTCTTCTCCAGAAATGTCCTCCATGACATACACGCTCGGGGGCA
|||||
CGAAATCTAGAAATC---TGCA
X
10
```



```
1540 1550 1560 1570 1580 1590 1600
AACCCATGTCATTCAGGGCGCTGAACCTTTCATCAGGATG-GAACAAAGTTGGCGTGCCTGAGACATATA
ATTCAAAGT--TCCAGAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
20 30 40 50 60 70 80

1610 1620 1630 1640 1650 1660 1670
TTTGGATACATTTGCCACAACACAGATGTCATTCATCACCATCTTCTGGCGCCAGCTAACTTTGTA
NNNG-NNNAT--CC-----CNGANTAGATTC-----TCTGTGT-----CTAAGATTCTTA
90 100 110 120 130

1680 1690 1700 1710 1720 1730 1740
CTGAAGCCTGGCCCATAGATTCGAACCATTCGAAGGCTTCACGTAATCTCCAAATATCAGGCTCTGA
--GATCAGATGCTCCA--AGATTCTAGATTTAAA-----TA-----AGATTCTAACGGTCTGT
140 150 160 170 180

1750 1760 1770 1780 1790 1800 1810 1820
TCCCACTCTCCACAGCTGTGGGTTTATCTGGTCTGAGGCTTTCGTCAAATCTGCTCAGACGCTTC
T--CTGT--TT-CAAGGCACTCTAGATTCAT-TGGTCC--AAGATTCCG--GATCCT-----AAGNATC
190 200 210 220 230

1830 1840 1850 1860 1870 1880
GCTGGG-CAAGCTC---TCCCAATGCTGTTCACCTCCATCACGCGAAGAGTAGTTCACGTAAGAGACA
NAAAGGANAGAGCNCACACNAGNNGGNNAGANANCAAGGNAATA-ANGTCNAANGNTGGACACC
240 250 260 270 280 290 300

1890 1900 1910 1920 1930 1940 1950
GCTTCAG-CTGGGCTGTGTCGTGT-TCCAGAAACCTTCAGTTTGGTGGCCACACCCCTGGCTTGTGCAT
NNTAGGCTCTTCTGCACTCTGCTCTAGGACCAT-GGTTAAG-AGTCCAGAAATCCACATTTCTAAA-
310 320 330 340 350 360 370

1960 1970 1980 1990 2000 2010 2020
TGCACTTTCATA-TTCGATG--ATGAATTTGTAATGGGCTATTTGTATCGCTGGGGTCCATGACAG
---ATCTT-ATAGTTCTAGCACTGTA-GTTCTAA-GACTCAAATGTTCTAAGTTTCTAAGATTC-TAA-AG
380 390 400 410 420 430 440

2030 2040 2050 2060 2070 2080 2090 2100
CTGAACACTTTTGTCAAGTTGATCTGTCACTTCTAGTCAAGGAGGATTTGGGACATCGTAAACGGGAGC
GTCCACA-----GGTCTAG-----ACTATTAGGTCAATTTCAAGG-----TTCTAAC--CCTATACTGTAGT
450 460 470 480 490

2110 2120 2130 2140 2150 2160 2170
TGGAGTTGGAGTAGGAGCACACGCTTAACACAGCGCTGGCGGAGACGCTGTCCAGAGTGGTGTGGCCAC
ATTCTTTGGGGT--GOCCTCTCCTTCTTAGC-TATC-ATTGCTTCTCTC-CTCCCCA-ACTG-----TGG-----
500 510 520 530 540 550

2180 2190 2200 2210 2220 2230 2240
ACAGGTGAGTCCCGCTGTCACTGTCATCGTCACTGATCACTACCTAGATG-ATCCTTGTCAACAG--TGAA
-----GGGT--GTGCCCT-TCA-AGCCTGTGCAAT--GC-ATTA-GGGATGCTCTCTTCCCGCAGGATGGA
560 570 580 590 600 610

2250 2260 2270 2280 2290 2300 2310
CCTTTCATCACTGGGAGTTCCTGTGTCTCTTCCAGCCA-CAGGACAGTGAAGGATAGGTGATCATGTT
CGATTTC--CACCTTTC-GGGCCATG-TGCCCGGAGCATCCGACCTTCTGAGA-NAGATGTGATC-TGGC
620 630 640 650 660 670 680

2320 2330 2340 2350 2360 2370
TCACTTTGCAATTCGAAGGACACCATGCTCCCTCTTTGCACAATGCAATTCGGGCTGTAAAGTGA
TCAAGGGGAGTCCA
690
X
```



```
PS      Example 4; SEQ ID NO 18916; 658pp + Sequence Listing; English.
XX      The present invention provides a number of single exon nucleic acid
CC      probes which are derived from genomic sequences expressed in the human
CC      bone marrow. They can be used to measure gene expression in bone marrow
CC      samples, which may enable the improved diagnosis and treatment of cancers
CC      such as lymphoma, leukaemia and myeloma. The present sequence is one of
CC      the probes of the invention
XX      Sequence 230 BP; 45 A; 61 C; 44 G; 80 T; 0 U; 0 Other;
SQ      AAK44359 Length: 230 July 26, 2004 14:10 Type: N Check: 7397
Initial Score = 71 Optimized Score = 111 Significance = 0.68
Residue Identity = 52% Matches = 139 Mismatches = 84
Gaps = 42 Conservative Substitutions = 0
420 430 440 450 460 470 480
GGAAGCGCTCATTAATTAACATCATGAGCGAGGAGAAAGCTGAGACCTATGAGAGTCTAT-CAGTGTACAGC
|||||
490 500 510 520 530 540 550
AAGGAACG-AACGCGAGCTGAGTTTCTAATAACATGTTTCCGCCCAICAGATCAC--CATGTGGAC
|||||
A--GAAGGTGCTCTGAGCTTTCGTTTC--CTTCAGCGGCTCT-TTCTCTTCTTACCACTGTATTGT---C
30 40 50 60 70 80
560 570 580 590 600 610 620
CAAGAAAACTTGAACCAATCACACTTCAAGTGTGTCAGTCTTTAGTACTTCCCTGCGAGACCCCAATTGG
|||||
C-AATTAAG-----GAGCC-ATC-CTCAATTGAAGTGGCCA---TTAACCCCTT--CTCCATA--GTCAACTAG
90 100 110 120 130 140
630 640 650 660 670 680 690
ATTACCAACCTATTAATTTTGGATGATTAATTCCTTTC--AAAGACTTCCACAAAGTGAGAGATTCTCT
|||||
GCTGTGTCGA-CTATCTTCTTTT---TTCA-CAGTCTCTGTCTGAAGGATTCGACTTCTCT-----TTTTT
150 160 170 180 190 200
700 710 720 730 740 750 760 770
C-AAGGTTGATGGGACCTTATTTTCCAAATGCTCTCCAGAGGACACCCGCGAGACTATATCTGTGA
|||||
CAAAGGCTTG--TGGTCTTCTGCAATCA
210 220 230
TGCTA
```

3. US-09-301-380-1 (1-4134)
aak44359 Human bone marrow expressed single exon probe SEQ

TOIG of: aak44359 check: 7397 from: 1 to: 230

```
ID      AAK44359 standard; DNA; 230 BP.
XX      Human bone marrow expressed single exon probe SEQ ID NO: 18916.
AC      AAK44359;
XX      Human; bone marrow expressed exon; gene expression analysis; probe;
XX      microarray; cancer; leukaemia; lymphoma; myeloma; ss.
OS      Homo sapiens.
XX      WO200157276-A2.
XX      09-AUG-2001.
XX      30-JAN-2001; 2001WO-US000668.
XX      04-FEB-2000; 2000US-0180312P.
XX      26-MAY-2000; 2000US-0207456P.
XX      30-JUN-2000; 2000US-00608408.
XX      03-AUG-2000; 2000US-00632366.
XX      21-SEP-2000; 2000US-0234687P.
XX      27-SEP-2000; 2000US-0236359P.
XX      04-OCT-2000; 2000GB-00024263.
XX      (MOLE-) MOLECULAR DYNAMICS INC.
XX      Penn SG, Hanzel DK, Chen W, Rank DR;
XX      WPI; 2001-488900/53.
XX      Human genome-derived single exon nucleic acid probes useful for analyzing
XX      gene expression in human bone marrow.
```

```
PS      Example 4; SEQ ID NO 18916; 658pp + Sequence Listing; English.
XX      The present invention provides a number of single exon nucleic acid
CC      probes which are derived from genomic sequences expressed in the human
CC      bone marrow. They can be used to measure gene expression in bone marrow
CC      samples, which may enable the improved diagnosis and treatment of cancers
CC      such as lymphoma, leukaemia and myeloma. The present sequence is one of
CC      the probes of the invention
XX      Sequence 230 BP; 45 A; 61 C; 44 G; 80 T; 0 U; 0 Other;
SQ      AAK44359 Length: 230 July 26, 2004 14:10 Type: N Check: 7397
Initial Score = 71 Optimized Score = 111 Significance = 0.68
Residue Identity = 52% Matches = 139 Mismatches = 84
Gaps = 42 Conservative Substitutions = 0
420 430 440 450 460 470 480
GGAAGCGCTCATTAATTAACATCATGAGCGAGGAGAAAGCTGAGACCTATGAGAGTCTAT-CAGTGTACAGC
|||||
490 500 510 520 530 540 550
AAGGAACG-AACGCGAGCTGAGTTTCTAATAACATGTTTCCGCCCAICAGATCAC--CATGTGGAC
|||||
A--GAAGGTGCTCTGAGCTTTCGTTTC--CTTCAGCGGCTCT-TTCTCTTCTTACCACTGTATTGT---C
30 40 50 60 70 80
560 570 580 590 600 610 620
CAAGAAAACTTGAACCAATCACACTTCAAGTGTGTCAGTCTTTAGTACTTCCCTGCGAGACCCCAATTGG
|||||
C-AATTAAG-----GAGCC-ATC-CTCAATTGAAGTGGCCA---TTAACCCCTT--CTCCATA--GTCAACTAG
90 100 110 120 130 140
630 640 650 660 670 680 690
ATTACCAACCTATTAATTTTGGATGATTAATTCCTTTC--AAAGACTTCCACAAAGTGAGAGATTCTCT
|||||
GCTGTGTCGA-CTATCTTCTTTT---TTCA-CAGTCTCTGTCTGAAGGATTCGACTTCTCT-----TTTTT
150 160 170 180 190 200
700 710 720 730 740 750 760 770
C-AAGGTTGATGGGACCTTATTTTCCAAATGCTCTCCAGAGGACACCCGCGAGACTATATCTGTGA
|||||
CAAAGGCTTG--TGGTCTTCTGCAATCA
210 220 230
TGCTA
```

4. US-09-301-380-1 (1-4134)
abs18595 Human genome-derived single exon probe ORF from lu

TOIG of: abs18595 check: 7397 from: 1 to: 230

```
ID      ABS18595 standard; DNA; 230 BP.
XX      Human genome-derived single exon probe ORF from lung SEQ ID No 18586.
AC      ABS18595;
XX      Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;
XX      chronic obstructive pulmonary disease; interstitial lung disease;
XX      familial idiopathic pulmonary fibrosis; neurofibromatosis;
XX      tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
XX      Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
XX      pulmonary histiocytosis; lymphangioma; lymphoma; Karagener syndrome;
XX      pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
XX      primary ciliary dyskinesia; pulmonary hypertension;
XX      hyaline membrane disease; open reading frame; ORF.
```

XX OS Homo sapiens.
 XX PN WO200186003-A2.
 XX PD 15-NOV-2001.
 XX PF 30-JAN-2001; 2001WO-US0000665.
 XX PR 04-FEB-2000; 2000US-0180312P.
 XX PR 26-MAY-2000; 2000US-0207456P.
 XX PR 30-JUN-2000; 2000US-0060840B.
 XX PR 03-AUG-2000; 2000US-00632366.
 XX PR 21-SEP-2000; 2000US-0234687P.
 XX PR 27-SEP-2000; 2000US-0236359P.
 XX PR 04-OCT-2000; 2000GB-00024263.
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2002-114183/15.
 XX Spatially-addressable set of single exon nucleic acid probes, used to
 XX measure gene expression in human lung samples.
 XX Claim 4; SEQ ID NO 18586; 634pp; English.
 XX The invention relates to a spatially-addressable set of single exon
 XX nucleic acid probes for measuring gene expression in a sample derived
 XX from human lung comprising single exon nucleic acid probes having one of
 XX 12614 nucleic acid sequences mentioned in the specification, or their
 XX complements or the 12387 open reading frames derived from the 12614
 XX probes. Also included are a microarray comprising the novel set of probes
 XX; the novel set of probes which hybridise at high stringency to a nucleic
 XX acid expressed in the human lung; measuring gene expression in a sample
 XX derived from human lung, comprising (a) contacting the array with a
 XX collection of detectably labeled nucleic acids derived from human lung
 XX mRNA, and (b) measuring the label detectably bound to each probe of the
 XX array; identifying exons in a eukaryotic genome, comprising (a)
 XX algorithmically predicting at least one exon from genomic sequences of
 XX the eukaryote; and (b) detecting specific hybridisation of detectably
 XX labeled nucleic acids from eukaryotic lung mRNA, to a single exon probe,
 XX having a fragment identical to the predicted exon, the probe is included
 XX in the above mentioned microarray; assigning exons to a single gene,
 XX comprising (a) identifying exons from genomic sequence by the method
 XX above and (b) measuring the expression of each of the exons in several
 XX tissues and/or cell types using hybridisation to a single exon
 XX microarrays having a probe with the exon, where a common pattern of
 XX expression of the exons in the tissues and/or cell types indicates that
 XX the exons should be assigned to a single gene; a peptide comprising one
 XX of 12011 sequences, mentioned in the specification, or encoded by the
 XX probes/open reading frames (ORF). The probes are used for gene expression
 XX analysis, and for identifying exons in a gene, particularly using human
 XX lung derived mRNA and for the study of lung diseases such as asthma, lung
 XX cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
 XX disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
 XX tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
 XX Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
 XX histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
 XX Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
 XX dyskinesia, pulmonary hypertension and hyaline membrane disease. The
 XX present sequence is a single exon probe open reading frame of the
 XX invention. Note: The sequence data for this patent did not form part of
 XX the printed specification, but was obtained in electronic format directly
 XX from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 230 BP; 45 A; 61 C; 44 G; 80 T; 0 U; 0 Other;
 XX ABS18595 Length: 230 July 26, 2004 14:11 Type: N Check: 7397 ..
 XX Initial Score = 71 Optimized Score = 111 Significance = 0.68
 XX Residue Identity = 52% Matches = 139 Mismatches = 84

Gaps = 42 Conservative Substitutions = 0
 420 430 440 450 460 470 480
 GGAACGCTCATAATTAACATCATGAGCGAAGGAAAGCTGAGACCTATGAGGAGTCTAT-CAGTGTACAGC
 |||||
 AGGAATTCATGCGCTTGACAGG X 10 20
 490 500 510 520 530 540 550
 AAGGAACG-AACGCGGAGCTGCATTTCTTAATACATGTTGTCCGCCATCCAGATCAC--CATTTGGAC
 |||||
 A--GAAGTGCTCTGAGCTTCTGTTTC-CTTACGCCGCTCT-TTCTCTTTTCTTACCAGTGTATGT---C
 30 40 50 60 70 80
 560 570 580 590 600 610 620
 CAAGAAAACTTGAACCAATCACACTTCAAGTGGTCACTTTAGTACTTCTCGAGACCCCAATTGG
 |||||
 C-AATAAAG---GAGCC-ATC-CTCATTTGAAGTGGCCA---TTAACCCCTT--CTCCATA--GTCAACTAG
 90 100 110 120 130 140
 630 640 650 660 670 680 690
 ATTACCAACCACTATATATTTGGATGGATATTCCTTTC--AAAGACTTCCAAAGTGAGAGATTCT
 |||||
 GCTGCTCCTCA-CATCTCTCTTTT---TTCACAGTCTCTGTGAAGGAGTTCGACTTCTCT-----TTTT
 150 160 170 180 190 200
 700 710 720 730 740 750 760 770
 C-AAGGTTTGAAGTGGGAGCTTTATTTTTCCTCCAGTCTCCAGAGACACCCCGAGACTATATCTGTTA
 |||||
 CAAGGCTTG--TGGTCTTCTGATCA 230
 210 220 230
 TGCTA
 5. US-09-301-380-1 (1-4134)
 abs44016 Human liver single exon probe, SEQ ID No 19006.
 TOIG of: abs44016 check: 7397 from: 1 to: 230
 ID ABS44016 standard; DNA; 230 BP.
 XX AC ABS44016;
 XX AC ABS44016;
 XX DT 25-FEB-2003 (first entry)
 XX DE Human liver single exon probe, SEQ ID No 19006.
 XX KW Human; single exon nucleic acid probe; liver; cirrhosis;
 XX KW hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
 XX KW coronary heart disease; ss.
 XX OS Homo sapiens.
 XX PN WO200157273-A2.
 XX PD 09-AUG-2001.
 XX PF 30-JAN-2001; 2001WO-US0000664.
 XX PR 04-FEB-2000; 2000US-0180312P.
 XX PR 26-MAY-2000; 2000US-0207456P.
 XX PR 30-JUN-2000; 2000US-0060840B.
 XX PR 03-AUG-2000; 2000US-00632366.
 XX PR 21-SEP-2000; 2000US-0234687P.
 XX PR 27-SEP-2000; 2000US-0236359P.
 XX PR 04-OCT-2000; 2000GB-00024263.
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2002-114183/15.

```
DR WPI; 2001-48898/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PS gene expression in human adult liver.
XX
XX Claim 4; SEQ ID NO 19006; 658pp; English.
XX
CC The invention relates to a single exon nucleic acid probe (SENP) (I) for
CC measuring human gene expression in a sample derived from human adult
CC liver, comprising one of 13109 defined nucleotide sequences given in the
CC specification (or complements/ fragments). The probe hybridises at high
CC stringency to a nucleic acid molecule expressed in the human adult liver.
CC (I) may be used for predicting, measuring and displaying gene expression
CC in samples derived from human adult liver. The genes identified may be
CC involved in genetic liver diseases such as cirrhosis,
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
CC associated with coronary heart disease. ABS25011-ABS51005 represent human
CC liver single exon nucleic acid probes of the invention. Note: The
CC sequence information for this patent does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pt_sequences
XX
SQ Sequence 230 BP; 45 A; 61 C; 44 G; 80 T; 0 U; 0 Other;
ABSA44016 Length: 230 July 26, 2004 14:11 Type: N Check: 7397
Initial Score = 71 Optimized Score = 111 Significance = 0.68
Residue Identity = 52% Matches = 139 Mismatches = 84
Gaps = 42 Conservative Substitutions = 0
420 430 440 450 460 470 480
GGAAGCGCTCATATTAACATCATGAGCGAAGGAGCTGAGACCTATGAGGAGTCTAT-CAGTGTACAGC
|||||
X 10
490 500 510 520 530 540 550
AAGGAACG-AACGCGGAGCTCAGTTCTTAATACATGTTGTCGCGCCATCCAGATCAC--CATTGTGGAC
|||||
A--GAAGTGCTGAGCTTCGTTTC-CTTCAGCCGGCTCT-TTCCTTTTACCACGTATTGT---C
30 40 50 60 70 80
560 570 580 590 600 610 620
CAAGAAACCTTGAACCAACACACTTCAAGTGGTCACTTTAGTCTCTGAGAGACCCCAATTGG
|||||
C-AATAAG-----GAGCC-ATC-CTCATGAACTGGCCA---TTAACCCCTT--CTCCATA--GTCAACTAG
90 100 110 120 130 140
630 640 650 660 670 680 690
ATTACCAACCTATAATATTTTGGATGGATAATTCCTTTC--AAAGACTTCCACAAAGTGAGAGATTCTT
GCTGTGCTCA-CTAATCTCTTTT---TTCA-CAGTCTGCTGGAAGGAGTTCGACTTCT-----TTTTT
150 160 170 180 190 200
700 710 720 X 730 740 750 760 770
C-AAGGTTTGAATGGGAGCCTTTATTTTTCGAATGCTCCAGAGGACACCCGGAGACTATATCTGTGA
|||||
CAAGGCTTG--TGTCTTCTGCAATCA
210 220 230
TGCTA
6. US-09-301-380-1 (1-4134)
aak45811 Human bone marrow expressed single exon probe SEQ
TOIG of: aak45811 check: 7602 from: 1 to: 224
ID AAK45811 standard; DNA; 224 BP.
XX
AC AAK45811;
XX
```

06-NOV-2001 (first entry)
Human bone marrow expressed single exon probe SEQ ID NO: 20368.
Human, bone marrow expressed exon; gene expression analysis; probe;
microarray; cancer; leukaemia; lymphoma; myeloma; ss.
Homo sapiens.
W0200157276-A2.
09-AUG-2001.
30-JAN-2001; 2001WO-US000668.
04-FEB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
(MOLE-) MOLECULAR DYNAMICS INC.
Penn SG, Hanzel DK, Chen W, Rank DR;
WPI; 2001-488900/53.
Human genome-derived single exon nucleic acid probes useful for analyzing
gene expression in human bone marrow.
Example 4; SEQ ID NO 20368; 658pp + Sequence Listing; English.
The present invention provides a number of single exon nucleic acid
probes which are derived from genomic sequences expressed in the human
bone marrow. They can be used to measure gene expression in bone marrow
samples, which may enable the improved diagnosis and treatment of cancers
such as lymphoma, leukaemia and myeloma. The present sequence is one of
the probes of the invention
SQ Sequence 224 BP; 58 A; 59 C; 49 G; 58 T; 0 U; 0 Other;
AAK45811 Length: 224 July 26, 2004 14:11 Type: N Check: 7602 ..
Initial Score = 38 Optimized Score = 107 Significance = -0.93
Residue Identity = 54% Matches = 134 Mismatches = 77
Gaps = 37 Conservative Substitutions = 0
2460 2470 2480 2490 2500 2510 2520
TACAAAGTTAGTGGCGCCAGAAAGANGGTGATGATGAATGACATCTGTGTTGTGCAATGTATCCA--
|||||
X 10 20
2530 2540 2550 2560 2570 2580 2590
AATATA-TTGCTCAGGACGCCAA-CCTTTGT--TCCA-TACCTGATCAAGTTCAGGCCCTGAATGACAT
|||||
ACTACAGCTGGCTGGG--GGCAAAACCCCATGTCATTGAGGGCCTGAACTTTGATCAGGTATGGA---ACA-
30 40 50 60 70 80
2600 2610 2620 2630 2640 2650 2660
GGGGTTTGC--CCCGAGCCAGCTGTAGTCAATGG-GACATTCTGGAGAGACCTCCCAATGTGCTCTCTGG
|||||
AAGGTTGGCGTGCCTGAGACA-ATATATT--TGATATATTGTCACAA-----CCACAGATG--TCCATT
90 100 110 120 130 140
2670 2680 2690 2700 2710 2720 2730
GAACGTGCGTGTGAATGGTGAACAG-TACCTTAG--CCGAGGTGCACTGGAGCCCACTACCTCTGAAAG
|||||
CATCATCACCATCTTCTGGCG-CCAGCTAACTTTGTACTGAAG-GC-CTGG--CCCATTAGAT--TCCAAAC
150 160 170 180 190 200 210

2740 X 2750 2760 2770 2780 2790
 CATCCGAGGACACCTACAGGCTATCGGATTTACTATTGGAGACCCAGAGTTCATCTAA
 |||||
 CATTCAGGG
 220 X

7. US-09-301-380-1 (1-4134)
 aba71469 Human foetal liver single exon nucleic acid probe
 TOIG of: aba71469 check: 7602 from: 1 to: 224

ID ABA71469 standard; DNA; 224 BP.
 XX AC ABA71469;
 XX AC
 DT 01-FEB-2002 (first entry)
 XX
 DE Human foetal liver single exon nucleic acid probe #19774.
 XX
 KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200157277-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000669.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 XX WPI; 2001-483447/52.
 DR
 PT Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human foetal liver.
 XX
 PS Claim 4; SEQ ID NO 19774; 639pp + Sequence Listing; English.
 XX
 CC The invention relates to a single exon nucleic acid probe for measuring
 CC human gene expression in a sample derived from human foetal liver. The
 CC single exon nucleic acid probes may be used for predicting, measuring and
 CC displaying gene expression in samples derived from human foetal liver. The
 CC present sequence is a single exon nucleic acid probe of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 224 BP; 58 A; 59 C; 49 G; 58 T; 0 U; 0 Other;

ABA71469 Length: 224 July 26, 2004 14:11 Type: N Check: 7602 ..

Initial Score = 38 Optimized Score = 107 Significance = -0.93
 Residue Identity = 54% Matches = 134 Mismatches = 77
 Gaps = 37 Conservative Substitutions = 0

2460 2470 2480 2490 2500 2510 2520
 TACAAGTAGCTGGGCCAGAAAGATGGTATGATGATGGACATCTGGTGTGGCAAAATGTATCCA--
 |||||
 TCCTTCCAGAATGT-CCCATG
 X 10 20

2530 2540 2550 2560 2570 2580 2590

AATATA-TTGCTCAGGCACGCCAA-CTTTGT--TCCA-TACCTGATCAAGTTTCAGGCCCTGAATGACAT
 |||||
 ACTACAGTGGCTCGGG--GGCAACCCCATGTCATTTCAGGCGCTGAACTTGATCAGTATGGA--ACA-
 30 40 50 60 70 80

2600 2610 2620 2630 2640 2650 2660
 GGGGTTTC--CCCGAGCCAGCTGTACTCATGG-GACATTCTGGAGAGACCTCCCAATGTGCTCCTGG
 |||||
 AAGGTGGCGTGGCTCGGACA-ATATATT--TGGATACATTTGCCACAA-----CCACAGATG--TCCATT
 90 100 110 120 130 140

2670 2680 2690 2700 2710 2720 2730
 GAACGTGCGTGTGAATGTGTGACAG-TACCTTAG--CCGAGGTGCACTGGGACCCAGTACCTCTGAAAG
 |||||
 CATATACCATCTTTCTGGCG-CCAGCTAACTTTGTACTGAAG-GC-CTGG--CCCATAGAT-TCGAAAC
 150 160 170 180 190 200 210

2740 X 2750 2760 2770 2780 2790
 CATCCGAGGACACCTACAGGCTATCGGATTTACTATTGGAGACCCAGAGTTCATCTAA
 |||||
 CATTCAGGG
 220 X

8. US-09-301-380-1 (1-4134)
 aa151738 TOIG of: aa151738 check: 8787 from: 1 to: 697

TOIG of: aa151738 check: 8787 from: 1 to: 697

LOCUS AA151738 697 bp mRNA linear EST 14-MAY-1997
 DEFINITION z128h03.r1 Soares pregnant_uterus_NbHPU Homo sapiens cDNA clone
 IMAGE:503285 5' similar to contains element MER22 repetitive
 element ;, mRNA sequence.

ACCESSION AA151738
 VERSION AA151738.1 GI:1720293
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 697)

REFERENCE

AUTHORS

Chisoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W.,
 Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
 Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,
 Mardis, E., Moore, S., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
 Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,
 Trevas, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R.
 and Marra, M.

Generation and analysis of 280,000 human expressed sequence tags
 Genome Res. 6 (9), 807-828 (1996)

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

Email: est@wustl.edu

This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 813 Std Error: 0.00

Seq primer: -28M13 rev2 from Amersham

High quality sequence stop: 513.

FEATURES

source

1..697
 /organism="Homo sapiens"
 /mol_type="mRNA"
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 /db_xref="taxon:9606"
 /clone="IMAGE:503285"
 /sex="female"
 /dev_stage="adult"
 /lab_host="DH10B"

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/clone_lib="soares_pregnant uterus NhPU"
/note="Organ: uterus; Vector: pT73-Pac; Site: 1: Not I;
Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer [5',
AAGCTGGAAGAAATTCGGCGCGCTTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization. Library
constructed by M. Fatima Bonaldo."

```

ORIGIN

AA151738 Length: 697 July 26, 2004 14:11 Type: N Check: 8787 ..

Initial Score	=	25	Optimized Score	=	294	Significance	=	-1.57
Residue Identity	=	46%	Matches	=	358	Mismatches	=	317
Gaps	=	100	Conservative Substitutions	=	0			

10 20 30 40 50 60 70
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 |||||
 CGAAANTCT-----AG
 X
 10

80 90 100 110 120 130 140
 AAAAGGAAATTCAGTGTGACGCTCAGCAG--GAGTTAAGCTAATGACGTTAAATAATGCCGAAAAAGA
 |||||
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TCCTTGATCCAAAACACTTCCTAGACACTGTGTACAGCTCCACACCTACCCCAACAGTCTCCAAAGATTACAT
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TATTGACCTCGGGAAATATT-GTAATCCACTGTGAGCCCAAGGAAACGGCCCCCAAGCTTTCCTG--
GATT--CCATTGTCGAATTCGGATCC--TAAGTATCAAGGAAAGAGCNCACACNAGNCGGGNN

360 370 380 390 400 410 420
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AGCCTCATATTAACA-TC-ATGAGCGAGGAAGCTGAGACCTATCAGGACTCTA-TCAGTGTACAGCA
AGGACCATGGTTAAGAGTCCAGAATCCA-CATTCTCTAAATCT-TATAG-TTCTAGGCATGTAGTTCT

0 500 510 520 530 540 550 560
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AAGACTCAA--ATGTTCT--AAGTTTCTAAGATCTCTAAAGTCCACAGCTCTAG---ACTATT--AGGTGCAAT
410 420 430 440 450 460 470

570 580 590 600 610 620 630
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TTCAAGGTT--CTAA---CCCTATACTGACT-ATTCTTT-GGGGTGCCCTTCCCTTCTTAGCTATCATTTG

	640	650	660	670	680	690	700
--	-----	-----	-----	-----	-----	-----	-----

CCACCCTATATAATTTTGGATGGATAAATTCCTTTCAAGACT--TCCACAAAGTAGAGAGATTCTTCAAGG
TTTGAATG--GGGACCTTT--ATTTC-----CAATGCTCCAGGACACCCGGGAAGACTATATCTGTTA
CCCGAGAGATGGACAGATCCACTTTCGGGCATGTG--CCCGA--GCATCCCC---AC--CTTCTG---
610 620 630 640 650 660
540 550 560 570 580 590 600 610

780 790 800 X 810 820 830 840
TGCTAGATTTAATCATATCTACATCAACCATACAGCAGAGCAACTATTCTGTGAGGTCATTTCAGTGGATCA
AGANAGATGTGATCTGGCTCAAGGGGNAGTCCA X

850
ATTGAATGACA